

SEQUENCE LISTING

<110> National Food Research Institute

<120> Erythrose Reductase, its cDNA and cell which the cDNA express

<130> P131238K

<160> 7

<210> 1

<211> 1119

<212> DNA

<213> Trichosporonoides megachiliensis

<400> 1

atg tct tac aaa cag tac atc ccc ctg aac gac ggt aac aaa atc cct 48

Met Ser Tyr Lys Gln Tyr Ile Pro Leu Asn Asp Gly Asn Lys Ile Pro

1 5 10 15

gcc ctt gga ttt ggt act tgg caa gct gaa cct ggt caa gtg ggt gca 96

Ala Leu Gly Phe Gly Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Ala

20 25 30

agt gtc aag aac gct gtc aag gct ggg tac cgt cat ttg gat ttg gcc 144

Ser Val Lys Asn Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala

35 40 45

aaa gtg tac caa aac caa tcg gaa att gga gta gca ctt cag gaa ctg 192

Lys Val Tyr Gln Asn Gln Ser Glu Ile Gly Val Ala Leu Gln Glu Leu

50 55 60

ttt gat caa ggt att gtt aaa cgg gaa gat ttg ttt att acg tcc aaa 240

Phe Asp Gln Gly Ile Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys

65 70 75 80

gta tgg aat aac cgt cat gct cct gaa cat gtt gag cct gca ttg gac 288

Val Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp

85 90 95

Leu Asn His Thr Pro Ala Ala Val Leu Leu Ala Trp Gly Ile Gln Arg
245 250 255
gga tac agt gta ttg gtc aag agt gtt aca cct tct cga att gag agc 816
Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Glu Ser
260 265 270
aat tat gat cag att acc ctt tct cct gaa gaa ttc cag aag gtt acg 864
Asn Tyr Asp Gln Ile Thr Leu Ser Pro Glu Glu Phe Gln Lys Val Thr
275 280 285
gat ttg atc aag gaa tat ggc gaa agt cgc aac aat att ccg ttg aat 912
Asp Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Ile Pro Leu Asn
290 295 300
tat aaa cct tca tgg ccc atc agt gtg ttt ggt aca tcg gat gaa gct 960
Tyr Lys Pro Ser Trp Pro Ile Ser Val Phe Gly Thr Ser Asp Glu Ala
305 310 315 320
aag gct act cat aag att aac acc aac ctt tga gttcagtttg ggaactatatt 1013
Lys Ala Thr His Lys Ile Asn Thr Asn Leu Stop
325 330
aaagctgctt gctggtcaca ttattgtcag tacctaccat gaagaattca atattatattt 1073
acattgtcaa ccattacatg gatccaaaaa aaaaaaaaaa aaaaaa 1119

<210> 2

<211> 1077

<212> DNA

<213> Trichosporonoides megachiliensis

<400> 2

atg tcc tac aac aag aac atc cct etc aac gac ggt aac tcc att cct 48
Met Ser Tyr Asn Lys Asn Ile Pro Leu Asn Asp Gly Asn Ser Ile Pro

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gct ctt ggg tac ggt acc tgg caa gca gaa cct ggt cag gtc ggt gaa				96
Ala Leu Gly Tyr Gly Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Glu				
20	25	30		
ggt gtc aag ctc gct gtt aag gct ggc tac cgt cat ttg gac ttg gcc				144
Gly Val Lys Leu Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala				
35	40	45		
aaa gta tac cag aac caa acc gag att ggc caa gct ctc aag gaa ctg				192
Lys Val Tyr Gln Asn Gln Thr Glu Ile Gly Gln Ala Leu Lys Glu Leu				
50	55	60		
ttt gat gag ggt gtt gtc aag cgt gag gac ctt ttc atc act tcc aag				240
Phe Asp Glu Gly Val Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys				
65	70	75	80	
ctt tgg aac aac cgc cac gct cct gag cac gtt gag cct gcg ctc gac				288
Leu Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp				
85	90	95		
gag act ctt aag gag ttg ggt cta tcc tat ttg gac ctg tac ttg att				336
Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile				
100	105	110		
cac tgg cct gtt gct ttc aag ttc act act ccc gat gaa ctg ctt cct				384
His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Asp Glu Leu Leu Pro				
115	120	125		
gct gac cct acc aac aag gac ctt gcc tac att gac gat tcg gtc aaa				432
Ala Asp Pro Thr Asn Lys Asp Leu Ala Tyr Ile Asp Asp Ser Val Lys				
130	135	140		
ttg tcc gac acc tgg aag gcg gtc gtc gcc ctg aaa aag acg ggt aag				480
Leu Ser Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys				
145	150	155	160	

acc aag tcg gtt ggt gtt tcg aac ttc agc act cgt ctg gtc gac ttg	528
Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu	
165 170 175	
gtt gag gaa gct tcg ggc gaa cgt cct gcg gtt aac cag atc gaa gct	576
Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala	
180 185 190	
cac ccc ttg ttg caa caa gac gag ttg gtt gct cac cat aag agc aag	624
His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys	
195 200 205	
aac att gtc atc act gct tac agt ccc ttg ggc aac aat gtc gct ggt	672
Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly	
210 215 220	
aaa cca cct ctg act gag aat ccc ggt att gtg gat gct gct aag cgt	720
Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg	
225 230 235 240	
ctg aac cat act cct gct gct gtg ctc att gct tgg ggt att caa cgc	768
Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg	
245 250 255	
ggg tac agc gtc ttg gtc aag tca gtt aca ccc tca cgg att aag agt	816
Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser	
260 265 270	
aac ttt gaa cag atc act ctg tct gat gag gaa ttc caa cgg gtt acc	864
Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr	
275 280 285	
aac ctc atc aag gag tac ggt gag agc cgt aac aac gtt cct ttc aac	912
Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn	
290 295 300	
tac aag cct tcg tgg tct att gac gtc ttt ggt acc cag tac gag gct	960

Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Tyr Glu Ala

305 310 315 320

aag gct acc cac aag att aac gct taa tgtgctctta tacaaaaagt 1007

Lys Ala Thr His Lys Ile Asn Ala Stop

325

cgtttgaacc tgtaatgtgt gaatgttate ctcattgttg catcatetca tcaaaaaaaaa 1067

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<210> 3

<211> 1121

<212> DNA

<213> Trichosporonoides megachiliensis

<400> 3

atg tcc tac aac aag aac atc cct ctc aac gac ggt aac tcc atc cct 48

Met Ser Tyr Asn Lys Asn Ile Pro Leu Asn Asp Gly Asn Ser Ile Pro

1 5 10 15

gcc ctt ggc tac ggt acc tgg caa gca gaa cct ggt cag gtc ggt gaa 96

Ala Leu Gly Tyr Gly Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Glu

20 25 30

ggt gtc aag ctc gct gtc aaa gct ggc tac cgt cac ttg gac ttg gcc 144

Gly Val Lys Leu Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala

35 40 45

aaa gtt tac cag aac caa acc gag att ggc caa gct ctc aag gaa ctg 192

Lys Val Tyr Gln Asn Gln Thr Glu Ile Gly Gln Ala Leu Lys Glu Leu

50 55 60

ttt gat gag ggt gtt gtc aag cgt gag gac ctt ttc atc act tcc aag 240

Phe Asp Glu Gly Val Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys

65	70	75	80	
ctt tgg aac aac cgc cac gct cct gag cac gtt gag cct gcg ctc gac				288
Leu Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp				
85	90	95		
gag act ctt aag gag ctg ggt cta tcc tat ctg gac ctg tac ttg att				336
Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile				
100	105	110		
cac tgg cct gtt gct ttc aag ttc act act ccc gat gaa ttg ctc cct				384
His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Asp Glu Leu Leu Pro				
115	120	125		
gct gac cct acc aac aag gat ctt gcc tac gtt gac gat tcg gta aaa				432
Ala Asp Pro Thr Asn Lys Asp Leu Ala Tyr Val Asp Asp Ser Val Lys				
130	135	140		
ttg tcc gac acc tgg aag gcg gtc gtc gcc ctg aag aag acg ggt aag				480
Leu Ser Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys				
145	150	155	160	
acc aag tcg gtt ggt gtt tcg aac ttc agc act cgt ctg gtc gac ttg				528
Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu				
165	170	175		
gtt gag gaa gct tcg ggc gaa cgt cct gcg gta aac cag atc gaa gct				576
Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala				
180	185	190		
cac ccc ttg ttg caa caa gac gag ttg gtt gct cac cat aag agc aag				624
His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys				
195	200	205		
aac att gtc atc act gct tac agt ccc ttg ggc aac aat gtc gct ggt				672
Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly				
210	215	220		

aaa cca cct ctg act gag aac ccc ggt att gtg gat gct gct aag cgt	720
Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg	
225 230 235 240	
ttg aac cat act cct gct gct gtg ctc att gct tgg ggt att caa cgc	768
Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg	
245 250 255	
ggg tac agc gtc ttg gtc aag tca gtt aca ccc tca cgg atc aag agt	816
Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser	
260 265 270	
aac ttt gaa cag atc act ctg tct gat gag gaa ttc caa cgg gtt acc	864
Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr	
275 280 285	
aac ctc atc aag gag tac ggt gag agc cgt aac aac gtt cct ttc aat	912
Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn	
290 295 300	
tac aag cct tcg tgg tcc att gac gtc ttt ggt acc cag gac gag gct	960
Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Asp Glu Ala	
305 310 315 320	
aag gct acc cac aag att aac gct taa tgtgctctta tacaaaaagt	1007
Lys Ala Thr His Lys Ile Asn Ala Stop	
325	
cgtttgaacc tgtaatgtgt gaatgttate ctcattgttg catcgtctca tcaaaaaaaaa	1067
aaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa aaaa	1121

<210> 4

<211>

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed nucleotide based on erythrose reductase type III
DNA sequence

<220>

<221> unsure

<222> 9

<223> n=a or c or g or t

<400> 4

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<210> 5

<211>

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed nucleotide based on erythrose reductase type III
DNA sequence

<220>

<221> unsure

<222> 3

<223> n=a or c or g or t

<220>

<221> unsure

<222> 18

<223> n=a or c or g or t

<400> 5

tgngcytcna tytgrttnac 20

<210> 6

<211>

<212> PRT

<213> Trichosporonoides megachiliensis

<400> 6

Gln Glu Leu Phe Asp Gln Gly

1

5

<210> 7

<211>

<212> PRT

<213> Trichosporonoides megachiliensis

<400> 7

Val Asn Gln Ile Glu Ala His

1

5